

FIG. 2A

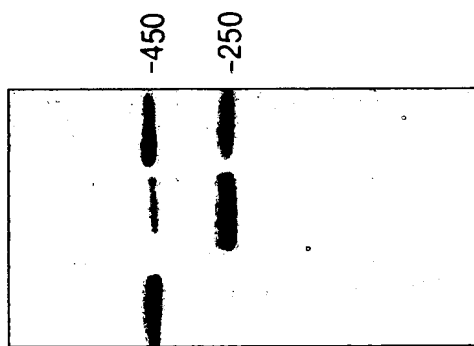
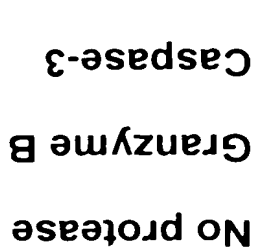


FIG. 2B

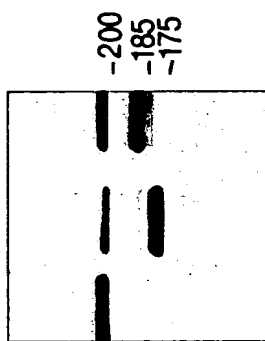
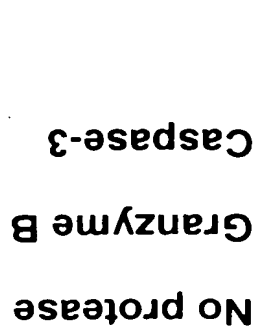


FIG. 2C

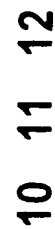
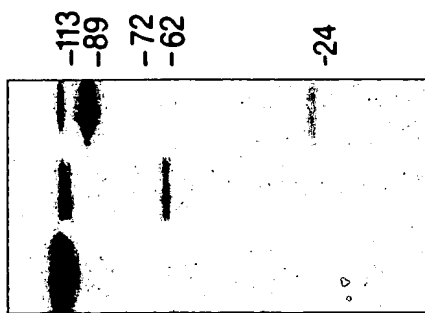
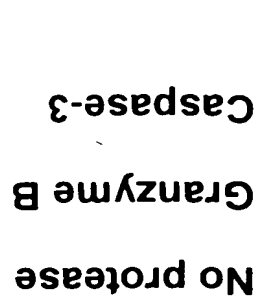


FIG. 2D

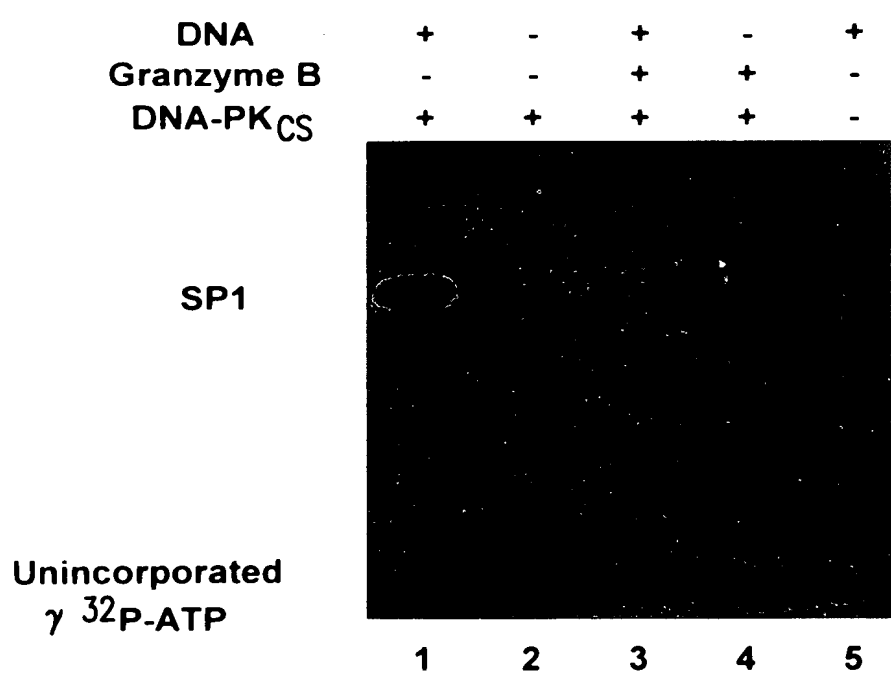


FIG.3

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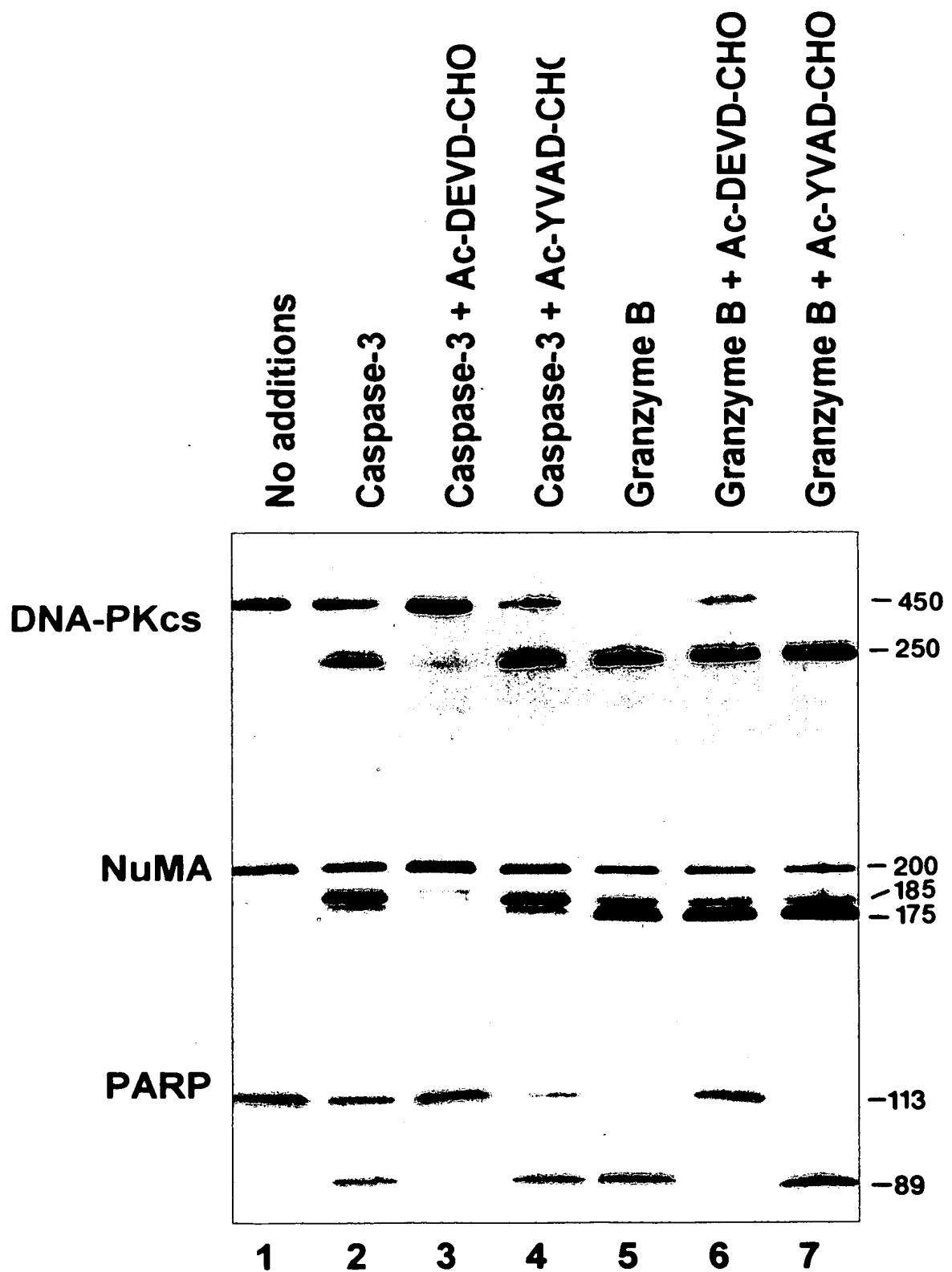


FIG.4

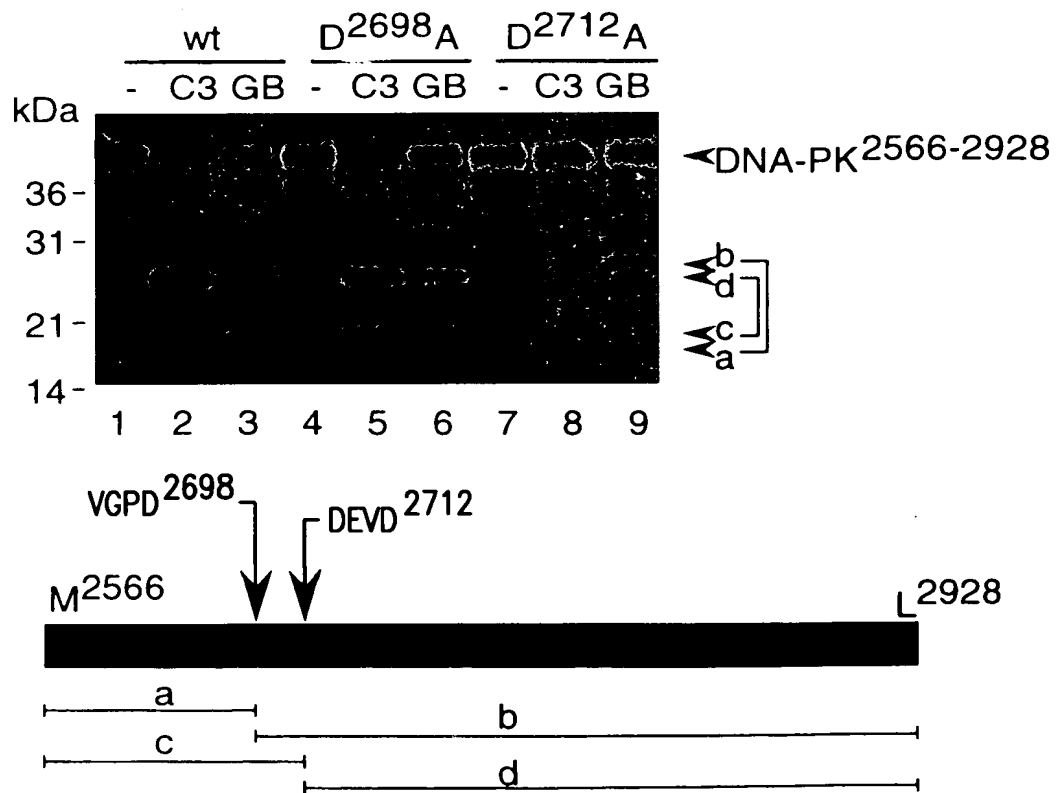
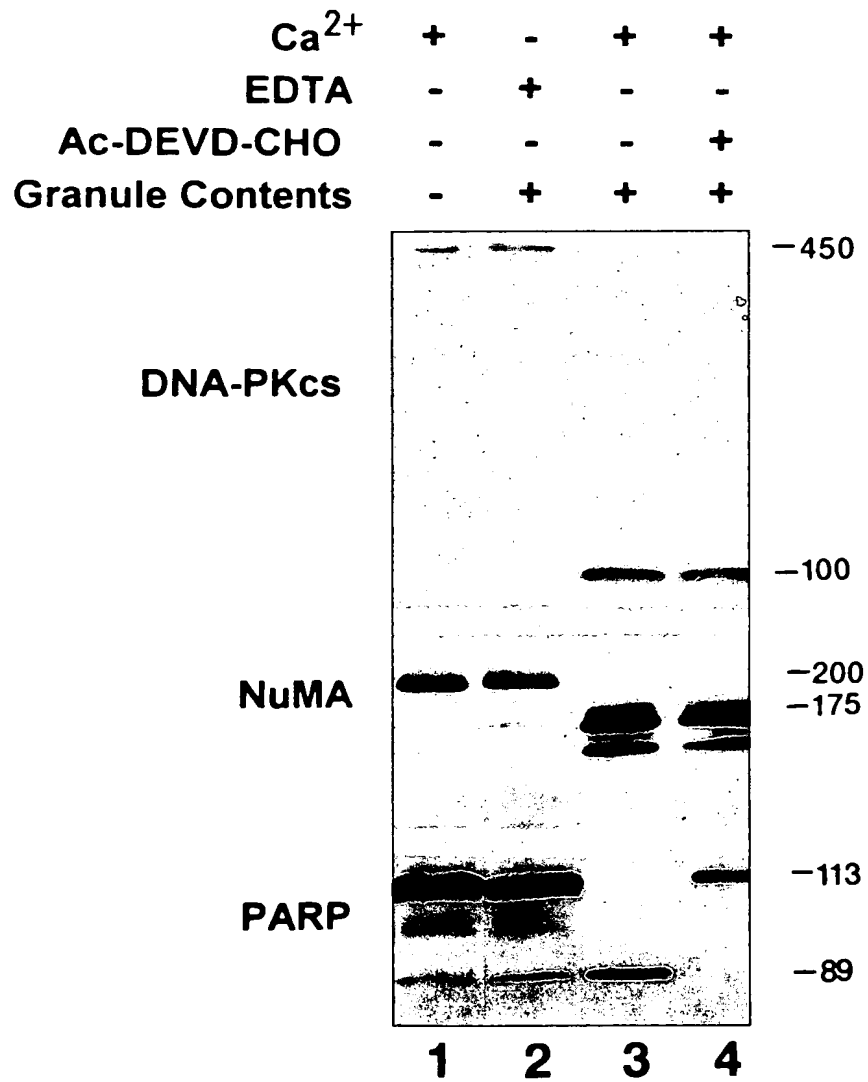


FIG.5

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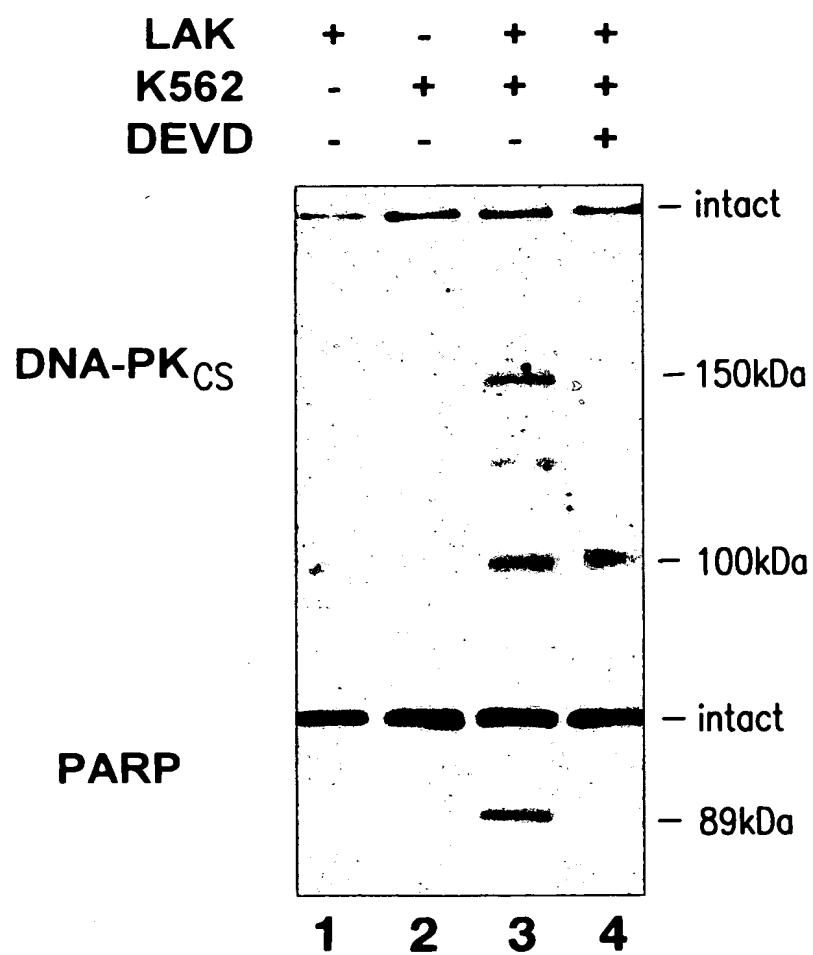


FIG.7

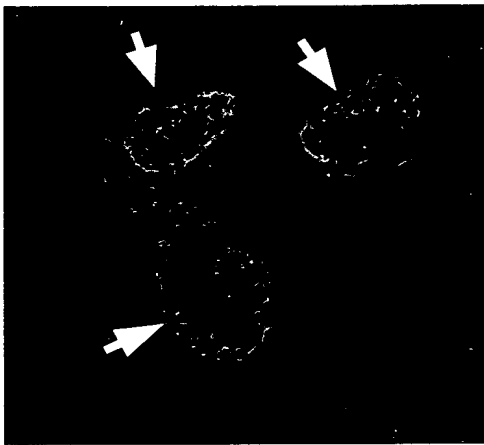


FIG. 8C



FIG. 8B



FIG. 8A

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LOCUS 284337 2101 aa 12-APR-1996
DEFINITION NuMA protein - human.
ACCESSION 284337
PID g284337
DBSOURCE PIR:locus A42184
summary: #length 2101 #molecular-weight 236296 #checksum 8715.
PIR dates: 31-Dec-1993 #sequence_revision 31-Dec-1993#text_change
12-Apr-1996.
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
REFERENCE 1 (residues 1 to 2101)
AUTHORS Compton,D.A., Szilak,I. and Cleveland,D.W.
TITLE Primary structure of NuMA, an intranuclear protein that defines a
novel pathway for segregation of proteins at mitosis
JOURNAL J. Cell Biol. 116 (6), 1395-1408 (1992)
MEDLINE 92176238
REFERENCE 2 (residues 1 to 2101)
AUTHORS Tang,T.K., Tang,C.J., Chen,Y.L. and Wu,C.W.
TITLE Nuclear proteins of the bovine esophageal epithelium.II. The NuMA
gene gives rise to multiple mRNAs and gene products reactive with
monoclonal antibody W1
JOURNAL J. Cell. Sci. 104 (Pt 2), 249-260 (1993)
MEDLINE 93280231
REFERENCE 3 (residues 1 to 2101)
AUTHORS Harborth,J., Weber,K. and Osborn,M.
TITLE Epitope mapping and direct visualization of the parallel,
in-register arrangement of the double-stranded coiled-coil in the
NuMA protein
JOURNAL EMBO J. 14 (11), 2447-2460 (1995)
MEDLINE 95300777
FEATURES Location/Qualifiers
source 1..2101
/organism="Homo sapiens"
/db_xref="taxon:9606"
Protein 1..2101
/product="NuMA protein"

FIG.9A

1 mtlhatrgaa llswvnslhv adpveavlql qdcsifikii drihgteegq qilqpvser
 61 ldfvcsflqk nrkhpsspec lvsqkvleg selelakmtm llyhstms ksprdweqfe
 121 ykiquaelavi lkfvldhedg lnlnedlenf lqkapvpstc sstfpeels pshqakreir
 181 flqlkvass ssgnnflsgs paspmgdilq tpqfqmrrlk kqladersnr delelelaen
 241 rklltekdaq iammqgridr lallnekqaa splekelee lrdknesltm rihetlkqcq
 301 dlkteksamd rkinqlseen gdlsfklref ashlaqlqda lnelttehs atqewlekqa
 361 qlekelmaal qdkkcleekn eilqgklsq eehlsqldn ppqekgevlq dvlqletlkq
 421 eaatlant qlgarvemle terqqeakl laerghfee kqqlsslitd lqssisnlsq
 481 akeeleqasq ahgarltaqv asltseittl natiqqdqe laglkqqake kqaqlaqlq
 541 qqeqasqglr hqveqlsssl kqkeqqlkev aekqeatrd haqqlatsae ereaslrerd
 601 aalkqleale kekaakleil qqqlqvanea rdsaqtsvtq aqrekaelsr kveelqacve
 661 tarqegheaq aqvaelql rseqqkatek ervaekdql qeqlqalkes lkvtkgslee
 721 ekrraadae eqqrciselk aetrlvegh krerkelee ragrkglear llqlgeahqa
 781 etevlrrela eamaaqhtae seceqlvkev aawrdgyeds qqeeaqgam fqeqlmtike
 841 eekarqelq eakekvagie shselqisrq qnklaelhan laralqqvqe kevraqklad
 901 dlstlqekma atskevarle tlvrkageqq etasrelvke paragdrqpe wleeqqgrqf
 961 cstqaalqam ereaegmgne lerlraalme sqqqaqeerg qqerevarlt qergraqadl
 1021 alekaarael emrlqnalne qrvefatlqe alahalteke gkdqelaklr glesaqikel
 1081 eelrqtvkql keglakkeke hasgsaqse aagrtptgp klealraevs kleqqcqkqkq
 1141 eqadslersl eaerasraer dsaletlqgq leekaqlgh sqsalasaqr elaafrtkvq
 1201 dhskaedewk aqvargrqea erknlissl eeevslnrq vlekegeske lkrlvmaese
 1261 ksqkleesca ccrqrqpatv pelqnaallc grrcrasgre aekgrvasen lrgeltsqae
 1321 raelqgelk awqekffqke qalstlqleh tstqalvsel lpakhlcaql qaeqaaekr
 1381 hreeleqskq aagglraell raqrelgeli plrqkvaee rtaqqlraek asyaeqlsmi
 1441 kkahgliae nrglgeranl grqfleveld qarekyvqel aavradaetr laevqreaqs
 1501 tarelevmta kyegakvkvl eerqrfqeer qltaqveel skkladsdqa skvqqqklka
 1561 vqaggesq eagrfqaqln elqaqlsake qaashyklqm ekakthydak kqqnqelqeq
 1621 lrsleqlake nkelraeae lghelqaggl kkeaeqtcr hltaqvrsle aqvahadaql
 1681 rdlgkfquat dalsrepqa kpqldlsids ldsceegtp lsitsklprt qpdgtsvpge
 1741 paspisqlp pkveslesly ftpiparsqa plessldslg dvfldsgrkt rsarrttqi
 1801 initmtkkld veepdsanss fystrsapas qaslratsst qslarlgspd ygnsallslp
 1861 gyrpttrssa rrsqagvssg appgrnsfym gtcqdepegd ddwnriaelq qnrvcpphl
 1921 ktcyplesrp slslgtitde emktgdpqet lrrasmapiq iaegtgittr qqrkrvslep
 1981 hqpgtpesk katscfprpm tprdrhegrk qstteaqqka apastkqadr rqsmefflln
 2041 tpkklgnsll rrgaskkals kaspntrsgt rrspriattd asaataaaig atprakgak
 2101 h

FIG.9B

LOCUS 107227 2115 aa10-NOV-1995
 DEFINITION NuMA protein - human.
 ACCESSION 107227
 PID gl07227
 DBSOURCE PIR: locus S23647
 summary: #length 2115 #molecular-weight 238273 #checksum 4391.
 PIR dates: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
 10-Nov-1995.
 KEYWORDS
 SOURCEhuman.
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
 Homo.
 REFERENCE 1 (residues 1 to 2115)
 AUTHORS Yang,C.H., Lambie,E.J. and Snyder,M.
 TITLE NuMA: an unusually long coiled-coil related protein in the
 mammalian nucleus
 JOURNAL J. Cell Biol. 116 (6), 1303-1317 (1992)
 MEDLINE 92176231
 FEATURES Location/Qualifiers
 source 1..2115
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 Protein 1..2115
 /product="NuMA protein"

FIG.10A

1 mtlhatrgaa llswvnslhv adpveavlql qdcsifikii drihgteegq qilqpvser
 61 ldfvcsflqk nrkhpsspec lvsaqkvleg selelakmtm lilyhstms ksprdweqfe
 121 ykiquaelavi lkfvldhedg lnlnedlenf lqkapvpstc sstfpeels pshqakreir
 181 flelqkvass sagnnflsgs paspmgdilq tpqfqrrik kqladersnr delelelaen
 241 rklltekdaq iammqgridr lallnekqaa splepkelee lrdknesltm rihetlkqcq
 301 dlkteksqmd rkinglseen gdlsfklref ashlaqlqda lnelttehs kCqewlekqa
 361 qlekelsaal qdkkcleekn eilqgklsq eehlsqldn ppqekgevlg dvlqletlkq
 421 eeatlaannt qlqarvemle terqqeakl laerghfeee kqqlsslitd lqssisnlsq
 481 akeeleqasq ahgarltaqv asltsettl natiqqdqde laglkqqake kqaqlaqlq
 541 qqeqasqglr hqveqlsssl kqkeqqlkev aekqeatrqd haqqlataae ereaslrerd
 601 aalkqleale kskaakleil qqqlqvanea rdsaqtsvtq aqrekaelsr kveelqacve
 661 tarqeqheaq aqvaelql rseqqkatek ervaqedql qeqlqalkes lkvtkgslee
 721 ekrraadae eqqrciselk aetrslveqh krerkelee ragrkglear lqqlgeahqa
 781 etevlrrela eamsaqhtae seceqlvkev aawreryeds qqeeaqygam fqeqlmtlke
 841 ecekarqelq eakekvagie shselgisrq qnelaelhan laralqqvqe kevrakqlad
 901 distlqekma atskevarle tlvrkageqq etasrelvke paragdrqpe wleeqqgrqf
 961 cstgaalgam ereaeqmne lerlraalme sqgqqqeerg qqerevarlt qergraqadl
 1021 alekaarael emrlqalne qrvefatlqe alahalteke gkdqelaklr gleaaqikel
 1081 eelrqtvkql keqlakkoke hasgsaqse aagrtptgp klealraevs kleqqcqkqkq
 1141 eqadslersl eaerasraer dsaletlqgq leekaqlgh sqsalasaqr elaafrtkvq
 1201 dhskaedewk aqvargrqea erknsissl eevesilnrq vlekegeske lkrivmaese
 1261 ksqkleerlr llaetasns araaerssal reevqslree aekqrvasen lrqeltsqae
 1321 raeelqgelk awqekffqke qalstlqleh tstqalvsel lpakhlcqql qaeqaaaekr
 1381 hreelegskq aagglraell raqrelgeli plrqkvaee rtaqqlraek asyaeqlsmi
 1441 kkahgliae nrglgeranl grqfleveld qarekyvqel aavradaetr laevqreaqs
 1501 tarelevmta kyegakvkvl eerqrfaeer qltaqveql evfqreatkq veelskklad
 1561 sdqaskvqqk klkavqaagg esqqaqrll aqlnelqaql sqkeqasehy klamekakth
 1621 ydakkqqnqe lqeqlrsloq lqkenkelra eaerlghelq qaglkkeae qtrhltaqv
 1681 rsleaqvaha dqqlrdlgkf qvatdalksr epqakpql d sidsldlsce egtplisitsk
 1741 lprtpdgtis vpgepaspis qrlppkvesl eslyftpipa rsqaplessl dslgdvfdqs
 1801 grktrsarrt ttqiinitmt kkldveepds anssfysters apasqasira tsstqslarl
 1861 gspdygnsal lslpgyrptt rssarrsqag vssgappgrn sfymgtcade peqlddwnri
 1921 aelqqrnrvc pphlktcyp l esrpslslgt itdeemktgd pqltllrasm qpiqiaegt
 1981 ittrqqrkrv slephqpgt peskkatscf prpmtprdrh egrkqsttea qkkaapastk
 2041 qadrrgsmaf silntpkklg nslrrgask kalskaspnt rsgtrrsprl atttasaata
 2101 aaigatprak gkakh

FIG.10B

LOCUS 1362789 4096 aa 06-SEP-1996
 DEFINITION DNA-activated protein kinase, catalytic subunit - human.
 ACCESSION 1362789
 PID g1362789
 DBSOURCE PIR:locus A57099
 summary: #length 4096 #molecular-weight 465420 #checksum 1795.
 genetic: #gene GDB:PRKDC ##cross-references GDB:234702
 #map_position 8q11.
 PIR dates: 27-Oct-1995 #sequence_revision 27-Oct-1995 text_change
 06-Sep-1996.
 KEYWORDS DNA binding; DNA recombination; DNA repair; nucleus;
 phosphotransferase.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Prunates; Catarrhini; Hominidae;
 Homo.
 REFERENCE 1 (residues 1 to 4096)
 AUTHORS Sipley, J.D., Menninger, J.C., Hartley, K.O., Ward, D.C., Jackson, S.P.
 and Anderson, C.W.
 TITLE Gene for the catalytic subunit of the human DNA-activated protein
 kinase maps to the site of the XRCC7 gene on chromosome 8
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92 (16), 7515-7519 (1995)
 MEDLINE 95365397
 REFERENCE 2 (residues 1 to 4096)
 AUTHORS Hartley, K.O., Gell, D., Smith, G.C., Zhang, H., Divecha, N.,
 Connelly, M.A., Admon, A., Lees-Miller, S.P., Anderson, C.W. and
 Jackson, S.P.
 TITLE DNA-dependent protein kinase catalytic subunit: a relative of
 phosphatidylinositol 3-kinase and the ataxia telangiectasia gene
 product
 JOURNAL Cell 82 (5), 849-856 (1995)
 MEDLINE 95401275
 FEATURES Location/Qualifiers
 source 1..4096
 /organism="Homo sapiens"
 /db_ef="taxon:9606"
 Protein 1..4096
 /note="DNA-PK-cs"
 /product="DNA-activated protein kinase, catalytic subunit"

FIG.11A

1 magsgagvrc slrlqetls aadrcgaala ghqlirglgq ecvlssspav lalqtslvfs
 61 rdfglivfvr kslnsiefre creeilkflc ifleRmgaki apysveiknt ctsvytkdra
 121 akckipaldi likllqtfrs srlmdefkig elfskfygel alkkkipdtv lekvyellgl
 181 lgevhpsemi nnaenlfrac lgelktqmts avrepklpvl agclkgllsl lcnftksmee
 241 dpgtsreifr fvlkairpqi dlkryavpsa glrlfalhas qfstclldny vsifevlikw
 301 cahtnvelkk aalsalesfl kvsnmvakn aemhknklqy emeqfygiir nvdsnnkels
 361 iairgyglfa gpokvinakd vdfmyveliq rckqmfltat dtgdyrvyam psflqsvasv
 421 llyldtvpv ytpvlehlvv mqidsfpqys pkmqlvccra ivkvflalaa kgpvlrncis
 481 tvvhqgliri cakpvvlpkg pesesedhra sgevrtgkwk vptykdyvdl frhlssdaqm
 541 mdsiladeaf fsvnsssesl nhllydefvk svlkivekld ltleiqtvgeq engdeapgv
 601 wmiptedpaa nlhpakpkdf safinlvefc reilpekqae ffepwvysfs yelilqstrl
 661 plisgyfkl sitvrnakki kyfegvspks lkhspedpek yscfalvkvf gkevavkmkq
 721 ykdellasci tflslphni ieldvrayvp alqmafklgl sytplaevgl naleewsiyi
 781 drhvmqpyyk dilpcldgyl ktsalsdetk nnwevsalsr aaqkgfnkvv lkhllkktkl
 841 ssneaislee irirvvqmlg slggqinknl lvtssdemm ksyvawdrek rlsfavpfre
 901 mkpvifldvf lprvtelalt asdrqtkvaa cellhsmvmf mlgkatampe ggggappmyq
 961 lykrtfpvll rladvdqvt rqlyeplvmq lihwftnnhk fesqdtvsll eaildgivdp
 1021 vdstlrdfcg rcireflkws ikaitpqaqe kspvntkslf krlyslalhp nafkrlgasl
 1081 afnniyrefr eeslveqfv fealviymes lalahadeks lgtiaqccda idhlcriiek
 1141 khvslnkakk rrlprgfpps aslclldlvk wllahcgrpq tecrhksiel fykfvplpg
 1201 nrspnlwkd vlkeegvsfl intfegggcg qpsgilagpt llylrgpfsi qatlcwldll
 1261 laalecyntf igertvgalq vlgteaqsll kavaffles iamhdiiae kcfgtgaagn
 1321 rtspqegery nyskctvvvr imefttlln tspegwkllk kdlcnthlmr vlvqtlcepa
 1381 sigfnigdvq vmahlpdvcv nlmkalkmsp ykdilethlr ekitaqsiee lcavnlygpd
 1441 aqvdrsrlla vvsackqlhr agllhnlps qstdlhhsvg tellslvykg iapgderqcl
 1501 psldlsckql asgllelafa fgglcerlvs lllnpavlst aslgssqgsv ihfshgeyfy
 1561 slfsetinte liknldlav elmqssvndt kmvsavlngm ldqsfreran qkhagklkl
 1621 tilqhwkkcd swwakdsple tkmavllalla kilgidssvs fntshgsfpe vfttyislla
 1681 dtklldhikg qavtlpfft sltggsleel rrvleqliva hfpmqsrefp pgtprfnnyv
 1741 dcmkkfldal elsqspmlle lmtvclreq qhvmeelfqs sfrriarrgs cvtqvglles
 1801 vyemfrkddp rlsftrqsfv drsltltlwh csldalreff stivvdaidv lksrftkline
 1861 stfdtqitkk mgyykildvm ysrlpkddvh akeskinqv hgscitegne ltktlklcy
 1921 daftenmage nqlerrrly hcaayncas vlcvfnelk fyqgflfsek peknllifen
 1981 lidlkrrynf pveevpmer kkyieirke areaangdsd gpsymsslsy ladstlseem
 2041 sqdfstgvq sysyssqdr patgrfrre qrdptvhddv lelemdelnr hecmaplal
 2101 vkhmbrslgp pqgeedsvpr dlpswmkflh gklgnpivpl nirlflaklv inteevfrpy
 2161 akhwslplq laasenngge gihymvveiv atilswtga tptgvpkdev lanrlnflm
 2221 khvfhpkrav frhnleikt lvecwkdcsl ipyrllfekf sgkdpnskdn svgiqllgiv
 2281 mandlppydp qcqigsseyf qalvnmefv rykevyaana evlgiliryv merknilees
 2341 lcelvakqlk qhantmedkf ivclnkvtks fppladrfrn avffllpkfh gvlktlclev
 2401 vlcrvegnte lyfqlkskdf vqvmhrder qkvcldiyyk mmpklkpvel relnppvfe
 2461 vshpsttcre qmynilmwih dnyrdpeset dndsqeifkl akdvliagli denpgqlii
 2521 rnfwshterl pentldrlla lnslyspkie vhlslatnf llemtsmspd ypnpmfehpl
 2581 secefqeyti dsdwrfrstv ltpmfvetqa sqgtlqtrtq egslsarwpv agqiratqq
 2641 hdtltqtad grssfdwtg sstdplvdht spssdsllfa hkrserlqra plksvgpdfg
 2701 kkrlglpgde vdnkvkgaag rtdllrlrrr fmrdaqeksl myarkgvaeg krekeiksel

FIG.11B

2761 kmkqdagvvl yrsyrhgdip diqikhssli tpiqavaqrd piiakqlfss lfsgilkemd
 2821 kfkltseknn itqklldfn rflnttfsff ppfvsciqdi scqhaallsi dpaavsagcl
 2881 aslqqpvgr lleeallrll paelpakrvr gkarlppdvl rwvelaklyr sigeydvirg
 2941 iftseigtkq itqsallaea rsdysesakq ydealnkqdw vdgepteak dfwelaslde
 3001 ynhaewksl eycstasids enppdlnkiw sepfyqetyl pymirsklkl llqgeadqsl
 3061 ltfidkamhg elqkailelh ysqelsllyl lqddvdraky yigngiqsfm qnyssidvll
 3121 hqsrltklqs vqalteiqef isfiskqgnl seqvplkrll ntwtnrypda kmdpmniwdd
 3181 iitnrcffls kieekltplp ednsmnvdqd gdpsdrmevq eqeedissli rsckfsmkmk
 3241 midsarkqnn fslamklke lhkesktrdd wlvswvqsy rishcrsrsg gcseqvltvl
 3301 ktvslldenn vssylxknll afrdqnilg ttyriianal ssepaclaei eedkarrile
 3361 lsgsssedse kviaglyqra fqlhseavqa aseeagppsw scgpaagvid aymtladfcg
 3421 qqlrkeeena svtdsaelqa ypalw ekml kalklnsnea rikfprllgi ierypeetls
 3481 lmtkeissvp cwqfiswish mvalldkdqa vavqhsveei tdnyppaivy pfiissesys
 3541 fkdttstghkn kefvariksk ldqggviqdf inalldqlnp ellfkdwsnd vraelaktpv
 3601 nkkniekmye rmyaalgdpk apglgafrrk fiqtfgkefd khfgkggskl lrmklsdnd
 3661 itnmlilkmn kdsppgnlk ecspwmsdfk veflrnelei pggydgrgkp lpeyhvirag
 3721 fdervtvmal lrrpkriir ghderhpfl vkggedlrqd qrveqlfqvm ngilaqdsac
 3781 sqralqlrty svvmtssdp rappceykdw ltkmsgkhdv gaymlmykga nrtetvtser
 3841 kreskvpadi lkrafvrmst speafalrs hfasshalic ishwiigig rhlnnfmvam
 3901 etggvigidf ghafgsatqf lvpelmpfr ltrqfinlml pmketglmys imvhalrafr
 3961 sdpgllntm dvfvkepsfd wknfeqkmlk kggswiqein vaeknwprq kicyakrkla
 4021 ganpavitcd elllghekap afrdyavar gskdhniaraq epesqlseet qvkcimdgat
 4081 dpnilgrtwe gwepwm

FIG.11C

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LOCUS 130781 1014aa 01-NOV-1997
DEFINITION POLY (ADP-RIBOSE) POLYMERASE (PARP) (ADPRT)
(NAD(+)
ADP-RIBOSYLTRANSFERASE) (POLY(ADP-RIBOSE)
SYNTHETASE).
ACCESSION 130781
PID gl30781
DBSOURCE SWISS-PROT: locus PPOL_HUMAN, accession P09874
class: standard.
created: Mar 1, 1989.
sequence updated: Dec 1, 1992.
annotation updated: Nov 1, 1997.
xrefs: gi: 510112, gi: 1017423, gi: 190166, gi: 190167, gi: 337423,
gi: 337424, gi: 178151, gi: 178152, gi: 190266, gi: 190267, gi:
178188, gi: 178190, gi: 189533, gi: 189534, gi: 35286, gi: 825702,
gi: 35288, gi: 189535, gi: 189536, gi: 88229, gi: 88227, gi:
627553, gi: 107162, gi: 107160, gi: 482956, gi: 420073, gi: 107158
xrefs (non-sequence databases): AAR;EUIS/GHENT-2DPAGE 1620,
MIM
173870, MIM 173871, PROSITE PS00347, PROSITE PS50064
KEYWORDS TRANSFERASE; GLYCOSYLTRANSFERASE; NAD; DNA-
BINDING; NUCLEAR
PROTEIN; ADP-RIBOSYLATION; ZINC-FINGER; ZINC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 1014)
AUTHORS Auer,B., Nagl,U., Herzog,H., Schneider,R. and
Schweiger,M.
TITLE Human nuclear NAD+ ADP-ribosyltransferase(polymerizing):
organization of the gene
JOURNAL DNA 8 (8), 575-580 (1989)
MEDLINE 90091744
REMARK SEQUENCE FROM N.A.
REFERENCE 2 (residues 1 to 1014)
AUTHORS Uchida,K, Morita,T., Sato,T., Ogura,T., Yamashita,R.,
Noguchi,S.,
Suzuki,H., Nyunoya,H., Miwa,M. and Sugimura,T.
TITLE Nucleotide sequence of a full-length cDNA for human fibroblast
poly(ADP-nbose) polymerase
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REMARK SEQUENCE FROM N.A.
TISSUE=FIBROBLAST

FIG.12A

1 maessdklyr veyaksgras ckkcsesipk dslrmainvq spmfdgkvph wyhfscfwkv
 61 ghsirhpdve vdgfseirwd dqqkvkktae aggvtkgqd gfgskaektl gdfaeyaks
 121 nrstckgcme kiekqvrls kkmvdpekpq lgmidrwyhp gcfvknreel gfrpeysasq
 181 lkgfslate dkealkkqlp gvksegkrkg devdgvdeva kkkskkekdk dsklekalka
 241 qndliwnkd elkkvcstnd lkellifnkq qvpegesail drvadgmvg allpceecag
 301 qlvfkedayy ctgdvtawtk cmvktqtpnr kewvtpkefr eisylkkikv kkqdrifppe
 361 tsasvaatpp pstasapaav nssasadkpl snmkiltlgk lsrnkdevka mieklggklt
 421 gtankasici stkkevekmn kkmeevkean irvvsedflq dvsastksiq elflahilsp
 481 wgaevkaepv evvaprgksg aalskkskgq vkeeginkse krmkltlkgg aavdpdagle
 541 hsahvlekkg kvfeatlplv divkgtnsyy klqlledcke nrywifrawg rvgtvigsnk
 601 legmpskeda iehfmklyee ktgnawhakn ftkypkkfyp leidyggdee avkkltvnpq
 661 tksklpkpvq dlikmifdve smkkamveye idlqkmpkg lskrqiaay silsevqqav
 721 sqgssdsqil dlsnrftli phdfgmkkpp llnnadsvqa kvemldnld ievaysllrg
 781 gsddsskdpi dvnyeklkt d ikvdrdsee aeirkyvkn thatthnayd levidifkie
 841 regecqrykp fkqlhnrll whgerttnfa gilaaglrta ppeapvtgym fgkgyfadm
 901 vsksanycht sqgdpiglil lgevalgnmy elkhaskisk lpkgkhsvkg lgkttpdpsa
 961 nislvgdvp lgtgissqvn dtsllyneyi vydiaqvnk yllklkfnfk tsw

FIG.12B